

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: September 4, 2002, 16:16:08 ; Search time 172.18 Seconds
(without alignments)
51.241 Million cell updates/sec

Title: US-09-052-089A-6

Perfect score: 293

Sequence: 1 LSLCTICSDFFDHSRDVAAL.....IOWFETAPSRTPCQRIOVG 51

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_19:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp-unclassified:*
15: sp-virus:*
16: sp-bacteriophage:*
17: sp-archaeoprotein:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	293	100.0	470	11	008854	008854 mus musculu
2	286	97.6	223	11	0922M8	0922M8 mus musculu
3	286	97.6	469	4	Q9BWF2	Q9BWF2 homo sapien
4	286	97.6	470	11	Q9CPA4	Q9CPA4 mus musculu
5	272	92.8	469	4	000467	000467 homo sapien
6	244	83.3	433	13	Q9YGN2	Q9YGN2 figu rubrip
7	128	43.7	435	5	Q95SS5	Q95SS5 drosophila
8	128	43.7	455	5	Q9V8D7	Q9V8D7 drosophila
9	127	43.3	310	10	082372	082372 arabidopsis
10	127	43.3	420	4	075866	075866 homo sapien
11	125	42.7	325	10	Q9M9U8	Q9M9U8 arabidopsis
12	124.5	42.5	263	5	Q95R85	Q95R85 drosophila
13	123	42.0	158	5	Q9XZS4	Q9XZS4 drosophila
14	115	39.2	327	11	Q9DHA2	Q9DHA2 mus musculu
15	115	39.2	349	10	Q947X9	Q947X9 oryza sativ
16	114	38.9	1181	5	097260	097260 plasmodium

17	113	38.6	224	10	Q9M9U7	Q9M9U7 arabidopsis
18	113	38.6	386	10	Q9LT14	Q9LT14 arabidopsis
19	112	38.2	304	5	Q9N3D1	Q9N3D1 caenorhabdi
20	112	38.2	344	10	065594	065594 arabidopsis
21	112	38.2	368	10	Q944I9	Q944I9 arabidopsis
22	112	38.2	383	10	Q9LMT3	Q9LMT3 arabidopsis
23	112	38.2	621	5	Q9V9T8	Q9V9T8 drosophila
24	112	38.2	626	5	Q95SP2	Q95SP2 drosophila
25	111	37.9	325	10	Q9LTU8	Q9LTU8 arabidopsis
26	110	37.5	274	10	Q9LZ10	Q9LZ10 arabidopsis
27	108	36.9	230	10	Q9FN35	Q9FN35 arabidopsis
28	108	36.9	489	5	Q9XUM8	Q9XUM8 caenorhabdi
29	107	36.5	137	4	Q9NSR1	Q9NSR1 homo sapien
30	107	36.5	396	10	Q9FM98	Q9FM98 arabidopsis
31	107	36.5	551	3	Q9H109	Q9H109 saccharomyc
32	107	36.5	879	13	Q90ZT8	Q90ZT8 gallus gall
33	107	36.5	923	13	Q90ZT7	Q90ZT7 xenopus lae
34	107	36.5	989	11	Q99ML9	Q99ML9 mus musculu
35	106.5	36.3	506	10	Q9M143	Q9M143 arabidopsis
36	106	36.2	367	10	Q9C9T6	Q9C9T6 arabidopsis
37	106	36.2	425	5	P90990	P90990 caenorhabdi
38	106	36.2	524	10	Q9M411	Q9M411 arabidopsis
39	105	35.8	590	5	Q95QK6	Q95QK6 caenorhabdi
40	105	35.8	1256	5	Q9VG16	Q9VG16 drosophila
41	104.5	35.7	441	10	Q23446	Q23446 arabidopsis
42	104	35.5	351	10	Q9ZVU8	Q9ZVU8 arabidopsis
43	102.5	35.0	237	10	Q9S1J7	Q9S1J7 arabidopsis
44	102.5	35.0	451	11	Q9CXX8	Q9CXX8 mus musculu
45	102.5	35.0	482	5	Q9VD21	Q9VD21 drosophila

ALIGNMENTS

RESULT 1
ID 008854 PRELIMINARY; PRT; 470 AA.
AC 008854;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE MTRIP.
GN TRAP OR MTRIP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97258620; PubMed=9104814;
RA Lee S.Y., Lee S.Y., Choi Y.;
RT "TRAF-interacting protein (TRIP): a novel component of the tumor
necrosis factor receptor (TNFR)- and CD30-TRAF signaling complexes
that inhibits TRAF2-mediated NF-kappaB activation.";
RL J. Exp. Med. 185:1275-1285(1997).
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: U77844; AAB52994.1; -
DR MGI: 1096377; Traip.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 470 AA: 53191 MW: 00FD705B52645133 CRC64;

Query Match 100.0%; Score 293; DB 11; Length 470;
Best Local Similarity 100.0%; Pred. No. 3.7e-31;
Matches 51; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSLCTICSDFFDHSRDVAALHCHGTFHLOCLLQWFTAPSRTPCQRIOVG 51
DB 4 LSLCTICSDFFDHSRDVAALHCHGTFHLOCLLQWFTAPSRTPCQRIOVG 54

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RESULT 2
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006929; AAH06929.1; -
SQ SEQUENCE 223 AA; 25584 MW; 412291C205C43071 CRC64;

Query Match
Best Local Similarity 97.6%; Score 286; DB 11; Length 223;
Pred. No. 1.5e-30; Mismatches 0; Indels 0; Gaps 0;
Matches 49; Conservative 1;

2 SLCTICSDPFDHSDVAIHGHTFHLCLOIOWFETAPSRTPCPCRIQVG 51
:|||||
5 ALCTICSDPFDHSDVAIHGHTFHLCLOIOWFETAPSRTPCPCRIQVG 54

RESULT 3
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; BC000310; AAH00310.1; -
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR ZINC-finger.
SQ SEQUENCE 469 AA; 53294 MW; B9EF3808F8C5985B CRC64;

Query Match
Best Local Similarity 97.6%; Score 286; DB 4; Length 469;
Pred. No. 3.2e-30; Mismatches 0; Indels 0; Gaps 0;
Matches 49; Conservative 1;

2 SLCTICSDPFDHSDVAIHGHTFHLCLOIOWFETAPSRTPCPCRIQVG 51
:|||||
5 ALCTICSDPFDHSDVAIHGHTFHLCLOIOWFETAPSRTPCPCRIQVG 54

RESULT 4
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006929; AAH06929.1; -
SQ SEQUENCE 223 AA; 25584 MW; 412291C205C43071 CRC64;

Query Match
Best Local Similarity 97.6%; Score 286; DB 11; Length 223;
Pred. No. 1.5e-30; Mismatches 0; Indels 0; Gaps 0;
Matches 49; Conservative 1;

2 SLCTICSDPFDHSDVAIHGHTFHLCLOIOWFETAPSRTPCPCRIQVG 51
:|||||
5 ALCTICSDPFDHSDVAIHGHTFHLCLOIOWFETAPSRTPCPCRIQVG 54

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GN TRAP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006929; AAH06929.1; -
SQ SEQUENCE 223 AA; 25584 MW; 412291C205C43071 CRC64;

Query Match
Best Local Similarity 97.6%; Score 286; DB 11; Length 470;
Pred. No. 3.2e-30; Mismatches 0; Indels 0; Gaps 0;
Matches 49; Conservative 1;

2 SLCTICSDPFDHSDVAIHGHTFHLCLOIOWFETAPSRTPCPCRIQVG 51
:|||||
5 ALCTICSDPFDHSDVAIHGHTFHLCLOIOWFETAPSRTPCPCRIQVG 54

RESULT 5
OS Mus musculus (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-1997) (Tremblrel. 04, Created)
DR EMBL; BC000310; AAH00310.1; -
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR ZINC-finger.
SQ SEQUENCE 470 AA; 53149 MW; EBFAB49A9F4BF2E CRC64;

Query Match
Best Local Similarity 97.6%; Score 286; DB 11; Length 470;
Pred. No. 3.2e-30; Mismatches 0; Indels 0; Gaps 0;
Matches 49; Conservative 1;

2 SLCTICSDPFDHSDVAIHGHTFHLCLOIOWFETAPSRTPCPCRIQVG 51
:|||||
5 ALCTICSDPFDHSDVAIHGHTFHLCLOIOWFETAPSRTPCPCRIQVG 54

RESULT 6
OS Mus musculus (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-1997) (Tremblrel. 04, Created)
DR EMBL; BC000310; AAH00310.1; -
DR InterPro; IPR001841; Znf_fing.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00184; RING; 1.
DR ZINC-finger.
SQ SEQUENCE 470 AA; 53149 MW; EBFAB49A9F4BF2E CRC64;

Query Match
Best Local Similarity 97.6%; Score 286; DB 11; Length 470;
Pred. No. 3.2e-30; Mismatches 0; Indels 0; Gaps 0;
Matches 49; Conservative 1;

2 SLCTICSDPFDHSDVAIHGHTFHLCLOIOWFETAPSRTPCPCRIQVG 51
:|||||
5 ALCTICSDPFDHSDVAIHGHTFHLCLOIOWFETAPSRTPCPCRIQVG 54

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DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 469 AA: 53138 MW: 2D54EDD04B64ABA64 CRC64;

Query Match 92.8%; Score 272; DB 4; Length 469;
Best Local Similarity 96.0%; Pred. No. 2.4e-28;
Matches 48; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 SLCTISDFDHSRDVAALHCGHTFHLQCLIQMFETAPSRTPCQCRIOVG 51
:|||||
DB 5 ALCTISDFDHSRDVAALHCGHTFHLQCLIQSFETAPSRTPCQCRIOVG 54

RESULT 6
O9YGN2 PRELIMINARY; PRT; 433 AA.

AC O9YGN2; 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE TRAF INTERACTING PROTEIN.
GN TRIP.
OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Takifugu.
OX NCBI_TaxID=31033;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99148833; PubMed-10025966;
RA Cottage A.J., Clark M., Hawker K., Umrantia Y., Wheller D., Bishop M., Elgar G.;
RT "Three receptor genes for plasminogen related growth factors in the genome of the puffer fish Fugu rubripes.";
RL FEBS Lett. 443:370-374(1999).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AJ010317; CAA09084.1; -
DR InterPro: IPR001841; Znf_Tfng.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 433 AA: 49201 MW: A8C31AAA4216E8C2 CRC64;

Query Match 83.3%; Score 244; DB 13; Length 433;
Best Local Similarity 83.0%; Pred. No. 1.2e-24;
Matches 39; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 4 CTTCSDFFDHSRDVAALHCGHTFHLQCLIQMFETAPSRTPCQCRIOVG 50
:|||||
DB 7 CTTCSDFFDHSRDVAALHCGHTFHLQCLIQMFETAPSRTPCQCRIOVG 53

RESULT 7
O9SSS5 PRELIMINARY; PRT; 435 AA.

AC O9SSS5; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GH03577P.
GN CG5140.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Plekoyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Y, CN BW SP;

RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunco J., Pacleb J., Paragas V., Park S., Phonanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Gelniker S.,
RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY060610; AAL28158.1; -
SQ SEQUENCE 435 AA: 48455 MW: 0BFF0AC81DD9416E CRC64;

Query Match 43.7%; Score 128; DB 5; Length 435;
Best Local Similarity 50.0%; Pred. No. 4.2e-09;
Matches 22; Conservative 6; Mismatches 14; Indels 2; Gaps 1;

QY 4 CTTCSDFFDHSRDVAALHCGHTFHLQCLIQMFETAPSRTPCQCR 47
:|||||
DB 6 CVCIAELFGQADVEFAFCVCGHMFHNCINQWLDLR--SKTCPCR 47

RESULT 8
O9Y8D7 PRELIMINARY; PRT; 455 AA.

AC O9Y8D7; 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CG5140. PROTEIN.
GN CG5140.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Plekoyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Branton R.C., Rogers Y.-H.C., Blazer J.R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfankuch C., Baldwin D.,
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter A., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Styckas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AEO03800: AAF57730.1; -
 DR FlyBase: FBgn0034314; CGS140.
 DR InterPro: IPR001841; ZnF_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 455 AA; 50726 MW; BEA74F4CACE8FD5B CRC64;

Query Match 43.7%; Score 128; DB 5; Length 455;
 Best Local Similarity 50.0%; Pred. No. 4.4e-09;
 Matches 22; Conservative 6; Mismatches 14; Indels 2; Gaps 1;

QY 4 CTICSDFFDHSRDVAIHCGHTFHLOCLQWETAPSRTPCQRIQV 47
 DB 6 CVICAELEFGADEVFATVCGHMFHNCINQWLDNR-SKTCPOCR 47

RESULT 9
 082372 PRELIMINARY; PRT; 310 AA.
 AC 082372;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE ATG2G9840 PROTEIN.
 GN ATG2G9840.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBL_TaxID=3702;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
 Beull C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 Cronin L.A., Shen M., Vanaken S.E., Uniyang L., Tallon L.J., Gail J.E.,
 Adams M.D., Carrera A.J., Creasy T.H., Gooden H.M., Somerville C.R.,
 R.A. Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*."
 RL Nature 402:761-768(1999).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AC005496; AAC35217.1; -
 DR HSSP: P28990; 1CHC.
 DR InterPro: IPR001841; ZnF_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 310 AA; 35390 MW; EEECL401152F5E2C CRC64;

Query Match 43.3%; Score 127; DB 10; Length 310;
 Best Local Similarity 41.7%; Pred. No. 4e-09;
 Matches 20; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

QY 3 LCTICSDFFDHSRDVAIHCGHTFHLOCLQWETAPSRTPCQRIQV 50
 DB 260 MCSICLEFDDGSRIVALPCGHEFDDECALUKWET--NHDCPLCRFLK 305

RESULT 10

075866 PRELIMINARY; PRT; 420 AA.
 AC 075866;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE R1343.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OC NCBL_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lameudin J.E., McCreedy P.M., Skowronski E., Viswanathan V.,
 Burkhardt-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
 Phan H., Velasco N., Do U., Regala W., Terry A., Barnes J.,
 Danganan L., Eiler A., Christensen M., Georgescu A., Avila J., Liu S.,
 Attix C., Andreise T., Frankheim M., Amico-Keller G., Coetfield J.,
 Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Krommiller B.,
 RA Arellano A., Saunders C., Ow D., Nolan M., Trong S., Kobayashi A.,
 Olsen A.S., Carrano A.V.;
 RT "Sequence analysis of a 2.5 Mb region in 19p13.3."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AC005764; AAC62428.1; -
 DR InterPro: IPR000561; EGF-like.
 DR InterPro: IPR003137; PA.
 DR InterPro: IPR001841; ZnF_ring.
 DR Pfam: PF02225; PA; 1.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 DR PROSITE: PS01186; EGF_2; UNKNOWNM_1.
 KW Zinc-finger.
 SQ SEQUENCE 420 AA; 45880 MW; 572731A8BA97FCE CRC64;

Query Match 43.3%; Score 127; DB 4; Length 420;
 Best Local Similarity 39.6%; Pred. No. 5.5e-09;
 Matches 19; Conservative 9; Mismatches 20; Indels 0; Gaps 0;

QY 3 LCTICSDFFDHSRDVAIHCGHTFHLOCLQWETAPSRTPCQRIQV 50
 DB 299 LCAICDEYEGQKLTPCSHTYHCKIDPWFSQAPRRSCPYCKQSV 346

RESULT 11

09M908 PRELIMINARY; PRT; 325 AA.
 AC 09M908;
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE F6A14.12 PROTEIN.
 GN F6A14.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBL_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,
 RA Altafi H., Araujo R., Huizar L., Rowley D., Buehler E., Dunn P.,
 RA Gonzalez A., Kremetska I., Kim C., Lenz C., Li J., Liu S.,
 RA Lueros S., Schwartz J., Shin P., Toriumi M., Vysotskaya V.S.,
 RA Walker M., Yu G., Ecker J., Theologis A., Davis R.W.;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AC011809; AAF27102.1; -
 DR InterPro: IPR001664; IF.
 DR InterPro: IPR001841; ZnF_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.

DR	SMAAT; SMO0184; RING; 1.
DR	PROSITE; PS00226; IF; UNKNOWN_1.
KW	Zinc-finger.
SO	SEQUENCE 325 AA; 36919 MW; 837FDB7F2B615 CRC64;
OY	Query Match Best Local Similarity 42.7%; Score 125; DB 10; Length 325; Matches 19; Conservative 11; Mismatches 16; Indels 2; Gaps 1;
Dd	3 LCTTCSDFDHSRDVAAIHCGHTFHQCLIQWFETAPSRKPCQRIOV 50 : :: ::: :: :: :: :: : Db VCTLLEEFDDGRSLVTLPCHGEPEECYLENF--VRSHVCPLCNLDEL 321
RESULT 12	
ID O95RBS PRELIMITARY; PRT; 263 AA.	
AC O95RB5	
DT 01-DEC-2001 (TREMBLrel. 19, Created)	
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DE LD4622IP.	
GN CG10916.	
OS Drosophila melanogaster (Fruit fly).	
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
OX Ephyrdoidea; Drosophilidae; Drosophila.	
XX NCBI_TaxID=7227;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=Y, CN BW SP,	
RA Stapleton M., Brokstein P., Hong L., Aghayani A., Carlson J.,	
RA Champe M., Chavez C., Dorsett V., Fafian D., Flise E., George R.,	
RA Gonzalez M., Guanin H., Li P., Liao G., Miranda A., Mungall C.J.,	
RA Nunooz J., Paclebo J., Paragas V., Park S., Phouanavong S., Wan K.,	
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;	
RL Submitted (OCT-2001) to the EMBL/GenBank/DDJB databases.	
DR EMBL; AY061504; AAL29052.1; -	
SQ SEQUENCE 263 AA; 29515 MW; B98CECE994071BFf CRC64;	
OY Query Match 42.5% ; Score 124.5; DB 5; Length 263; Best Local Similarity 48.9%; Pred. No. 7.4e+09; Matches 23; Conservative 6; Mismatches 13; Indels 5; Gaps 3;	
Dd	3 ICTTCSDFFDHSRDV-AAIHCGHFTFLQCLOWETAAPSRTCPOCR 47 :: :: : : :: :: :: Db LCATICNEFF-RANDITIFSTRGCVHFHKDCILRWLNLR-SRKCPCKOR 74
RESULT 13	
ID O9XZS4 PRELIMITARY; PRT; 158 AA.	
AC O9XZS4	
DT 01-NOV-1999 (TREMBLrel. 12, Created)	
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)	
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)	
DE EG:22E5.12 PROTEIN.	
GN EG:22E5.12 OR CG4325	
OS Drosophila melanogaster (Fruit fly).	
OC Pterygota; Melazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	
CC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;	
CC Ephyrdoidea; Drosophilidae; Drosophila.	
OX NCBI_TaxID=7227;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=BKKELBY;	
RA MEDLINE=20196006; PubMed=10731132;	
RA Adams M.D., Celinkner S.E., Holt R.A., Evans C.A., Gocayne J.D.,	
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,	
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,	
RA Sutton G.G., Wortman J.R., Landell M.D., Zhang Q., Chen L.X.,	

[illegible]

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi T., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamazaki I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carinici P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gerbaldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.,
RT Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AK005843; BAB24269.1; -.
DR HSSP: P28990; ICNC.
DR MGD: MG1:1341258; Ssrzf1.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00097; zf-C3HC4.1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
KW Zinc-finger.
SQ
SEQUENCE 327 AA; 35627 MW; 5F8D34ABFE394193 CRC64;

Query Match 39.2%; Score 115; DB 11; Length 327;
Best Local Similarity 35.4%; Pred. No. 1.7e-07;
Matches 17; Conservative 9; Mismatches 22; Indels 0; Gaps 0;

QY 3 LCTICSDPFDSRDVAIHCGRFHLCQLIQWFTAPSRTPCPCRIQV 50
DB 208 LCAICLDYIEGERTKILPCAHAYHCRCIDPWFSAQRSCPLCKQSV 255

RESULT 15
Q947X9 PRELIMINARY: PRT; 349 AA.
AC Q947X9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 39.6 KDA PROTEIN.
GN OSJNBA0067N01.18.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NIPPONBARE;
RA de la Bastide M., Spiegel L., Preston R., Kirchoff K., King L.,
RA Nascimben L., Baker J., Vil M.D., Zulaevan T., Santos L., Miller B.,
RA Kuit K., Cunnius D.M., Rodriguez S., Balija V., Shah R., Bahret A.,
RA Yang C., Bell M., Palmer L., O'Shaughnessy A., Dedhia N.,
RA McCombie W.R.,
RT Genomic Sequence for Oryza sativa, Nipponbare strain, clone
OSJNBA0067N01, from chromosome 3, complete sequence.";

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RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC090485; AAK98739.1; -.
KW Hypothetical protein
SQ SEQUENCE 349 AA; 39557 MW; ECF2CDC80C2E2DB1 CRC64;

Query Match 39.2%; Score 115; DB 10; Length 349;
Best Local Similarity 40.9%; Pred. No. 1.8e-07;
Matches 18; Conservative 12; Mismatches 12; Indels 2; Gaps 2;

QY 4 CTICSDPFDSRDVAIHCGRFHLCQLIQWFTAPSRTPCPC 46
DB 212 CPVCFEYLFSTFDISALHCGRTHIECLYE-MRSHQFSCPYC 254

RESULT 16
Q97260 PRELIMINARY: PRT; 1181 AA.
AC Q97260;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 135.6 KDA PROTEIN.
GN PFC0610C; MAL3P5.8.
OS Plasmodium falciparum (Isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=99376085; PubMed=10448855;
RA Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA Churcher C.M., Craig A., Davies R.M., Devlin K., Feltham T.,
RA Gentles S., Galloway R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
RA Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA Whitehead S., Woodward J.R., Newbold C., Barrell B.G.,
RT The complete nucleotide sequence of chromosome 3 of Plasmodium
falciparum.";
RL Nature 400:532-538(1999).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AL034556; CAB38971.1; -.
DR HSSP: P28990; ICNC.
DR InterPro: IPR001841; ZnF_ring.
DR Pfam: PF00097; zf-C3HC4.1.
DR SMART: SM00184; RING; 1.
KW Hypothetical protein; Zinc-finger.
SQ SEQUENCE 1181 AA; 135638 MW; 288C44EA4FB8C2D4 CRC64;

Query Match 38.9%; Score 114; DB 5; Length 1181;
Best Local Similarity 36.0%; Pred. No. 8.4e-07;
Matches 18; Conservative 12; Mismatches 18; Indels 2; Gaps 1;

QY 1 LSLCTICSDPFDSRDVAIHCGRFHLCQLIQWFTAPSRTPCPCRIQV 50
DB 1128 LKKCCICGCGYQNDVNIPLPCTHNFHKCCILKWI--SKNTTGPLCKIDL 1175

RESULT 17
Q9M9U7 PRELIMINARY: PRT; 224 AA.
AC Q9M9U7;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F6A14.13 PROTEIN.
GN F6A14.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.

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Query Match      38.6%;   Score 113;   DB 10;   Length 386;
Best Local Similarity 36.0%;   Pred. No. 3.8e-07;
Matches 18; Conservative 9; Mismatches 21; Indels 2; Gaps 1.

QY 1 LSLCTICDSFDHSDVAALHCGHFFHLOCLLQWETASRRCPOCRIOY 50
   :: : : : : : : : : : : : : : : : : : : : : : : : :

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RL Submitted (MAR-1998) to

RA Mewes

RP SEQUENCE FROM N.A.
RA Beyan M., Vandenbol M., Jallet C., Portetelle D., Hohensei J.,
RA Mewes H.W., Mayer K., Schueller C.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE OF 65-344 FROM N.A.
 RA Rose M., Hempel S., Ertlan K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Vandenbol M., Jallet C., Portetelle D., Mewes H.W., Lemcke K.,
 RA Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AL022223; CA18230.1; -;
 DR EMBL: AL161565; CAB79495.1; -;
 DR InterPro: IPR001841; Znf_1ing.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Hypothetical protein; Zinc-finger.
 SQ SEQUENCE 344 AA; 38720 MW; EB31D0BF5EDA700 CRC64;

Query Match 38.2%; Score 112; DB 10; Length 344;
 Best Local Similarity 38.3%; Pred. No. 4.6e-07;
 Matches 18; Conservative 9; Mismatches 18; Indels 2; Gaps 1;

OY 4 CTTCSDFFDHSRDVAAIHCGHTFHLQCLIQWFTAPSRTPCQCR 50
 Db 229 CSICDDEYERDEYGEINCGSHFHCVKQWL--SRKNACPVCK 273

RESULT 21
 ID 0944L9 PRELIMINARY; PRT; 368 AA.
 AC 0944L9;
 DT 01-DEC-2001 (TREMblrel. 19, Created)
 DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE ATG1G1970/F2H15.16
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carlincl P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones."
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF28290; AAL16122.1; -;
 SQ SEQUENCE 368 AA; 41618 MW; 79AD48BD0790A08E CRC64;

Query Match 38.2%; Score 112; DB 10; Length 368;
 Best Local Similarity 36.4%; Pred. No. 4.9e-07;
 Matches 16; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

OY 4 CTTCSDFFDHSRDVAAIHCGHTFHLQCLIQWFTAPSRTPCQCR 47
 Db 320 CSICDDEYERDEYGEINCGSHFHCVKQWL--SRKNACPVCK 361

RESULT 22
 ID 09LMT3 PRELIMINARY; PRT; 383 AA.

AC 09LMT3;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE F2H15.19 PROTEIN.
 GN F2H15.19.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA Sakano H., Liu S.X., Etgu P., Lee J.M., Lenz C., Pham P., Toriumi M.,
 RA Yu G., Chan A., Chung M., Goldsmith A., Liu A., Smith A., Vaysberg M.,
 RA Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B.,
 RA Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M.,
 RA Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R.,
 RA Federspiel N.A., Theologis A.;
 RT "The sequence of BAC F2H15 from Arabidopsis thaliana chromosome 1."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AC034106; AAF97276.1; -;
 DR InterPro: IPR001841; Znf_1ing.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 383 AA; 43262 MW; EE8ADE91FE0B224 CRC64;

Query Match 38.2%; Score 112; DB 10; Length 383;
 Best Local Similarity 36.4%; Pred. No. 5.1e-07;
 Matches 16; Conservative 11; Mismatches 15; Indels 2; Gaps 1;

OY 4 CTTCSDFFDHSRDVAAIHCGHTFHLQCLIQWFTAPSRTPCQCR 47
 Db 335 CSICDDEYERDEYGEINCGSHFHCVKQWL--SRKNACPVCK 376

RESULT 23
 ID 09V9T8 PRELIMINARY; PRT; 621 AA.
 AC 09V9T8;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE CG1937 PROTEIN.
 GN CG1937.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazek R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA April J.F., Agbayani A., An H.-J., Andrews-Plankoch C., Baldwin D.,
 RA Bailley R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies S.M.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabriellian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodak A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Houtin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
 RA Jatalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matzel B., McIntosh T.C., McLeod M., McPherson D.,
 RA Merkulov G., Mishina N.V., Moberly C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Swirski R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AB003779; AAF57196.1; -.
 DR FLYbase: FBgn0039875; CG1937.
 DR InterPro: IPR001841; ZnF_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW ZINC-finger.
 SQ SEQUENCE 621 AA; 68752 MW; ABDEB1609E2C0A1 CRC64;

Query Match 38.2%; Score 112; DB 5; Length 621;
 Best Local Similarity 40.0%; Pred. No. 8.2e-07;
 Matches 20; Conservative 9; Mismatches 15; Indels 6; Gaps 3;
 Y 2 SLCTIC-SDFDHSRDVAALHCGHTFHLQCLIQWFTAPSRTPCQCRIOV 50
 Db 278 NITLICREDVNVNSK---KLPCGHITHTCLRSMFOR--QQTCTPCLRLNI 322

RESULT 24
 ID 095SP2 PRELIMINARY; PRT; 626 AA.
 AC 095SP2;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE GH11117P.
 GN CG1937.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_Taxid=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=; CN BW SP;
 RA Stapleton M., Broksstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Garin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Pacleb J., Paragas V., Park S., Phuananavong S., Wan K.,
 RA Xu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY060677; AAL28225.1; -.
 SQ SEQUENCE 626 AA; 69272 MW; F881B88D51D724EC CRC64;

Query Match 38.2%; Score 112; DB 5; Length 626;
 Best Local Similarity 40.0%; Pred. No. 8.3e-07;
 Matches 20; Conservative 9; Mismatches 15; Indels 6; Gaps 3;

Y 2 SLCTIC-SDFDHSRDVAALHCGHTFHLQCLIQWFTAPSRTPCQCRIOV 50
 Db 287 NITLICREDVNVNSK---KLPCGHITHTCLRSMFOR--QQTCTPCLRLNI 331

RESULT 25
 ID 09LTU8 PRELIMINARY; PRT; 325 AA.
 AC 09LTU8;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-DEC-2000 (TREMBLrel. 15, last sequence update)
 DE GH1AAE27103.1.
 OS *Arabidopsis thaliana* (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COLUMBIA;
 RX MEDLINE=20277480; PubMed=10819329;
 RA Nakamura Y.;
 RT "Structural analysis of *Arabidopsis thaliana* chromosome 3. I. Sequence
 RT features of the regions of 4,504,864 bp covered by sixty P1 and YAC
 RT clones.";
 RL DNA Res. 7:131-135(2000).
 CC -I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL: AB024034; BAB02789.1; -.
 DR HSSP: P28990; ICHC.
 DR InterPro: IPR001841; ZnF_ring.
 DR Pfam: PF00097; zf-C3HC4; 1.
 DR SMART: SM00184; RING; 1.
 KW ZINC-finger.
 SQ SEQUENCE 325 AA; 36432 MW; 694044F361053DE4 CRC64;

Query Match 37.9%; Score 111; DB 10; Length 325;
 Best Local Similarity 40.4%; Pred. No. 5.9e-07;
 Matches 19; Conservative 10; Mismatches 16; Indels 2; Gaps 1;
 Y 4 CTICSDFFDHSRDVAALHCGHTFHLQCLIQWFTAPSRTPCQCRIOV 50
 Db 275 CTICLEEFNAGILVALPCGHDDECAVKWFT--NHFCPLCRYEL 319

RESULT 26
 ID 09L210 PRELIMINARY; PRT; 274 AA.
 AC 09L210;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-DEC-2000 (TREMBLrel. 15, last sequence update)
 DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)
 DE HYPOTHETICAL 31.1 KDA PROTEIN.
 GN F9G14.60.
 OS *Arabidopsis thaliana* (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_Taxid=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Terryn N., Ardiles W., Buyschaert C., Dasseville R.,
 RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
 RA Villarroel R., Glejen J., Van Montagu M., Bancroft I., Mewes H.W.,
 RA Rudd S., Lemcke K., Mayer K.F.X.;
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]

RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AL162973; CAB86029.1; -.
DR InterPro: IPR001841; Znf_1ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Hypothetical protein; zinc-finger.
SQ SEQUENCE 274 AA; 31102 MW; 9A98B6C495A6F068 CRC64;

Query Match 37.5%; Score 110; DB 10; Length 274;
Best Local Similarity 38.3%; Pred. No. 6.7e-07;
Matches 18; Conservative 7; Mismatches 20; Indels 2; Gaps 1;

OY 4 CTCGSEDFHSRDVAAIHCGHTFHLOCLIQWFEFAFSRTCPQCRIOY 50
DB 205 CVICKESMSEGRDVCMPCHQHFHMKCILPWL--SKKNTCPFCRFOL 249

RESULT 27
O9FN35 PRELIMINARY; PRT; 230 AA.

AC O9FN35;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE GB|AAFP27103.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA MEDLINE=98162728; PubMed=9501997;
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RT physically assigned pl clones."
RL DNA Res. 4:401-414(1997).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AB007644; BAB10721.1; -.
DR InterPro: IPR001841; Znf_1ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 230 AA; 26799 MW; 4033546C9C5FC72 CRC64;

Query Match 36.9%; Score 108; DB 10; Length 230;
Best Local Similarity 38.3%; Pred. No. 1e-06;
Matches 18; Conservative 9; Mismatches 18; Indels 2; Gaps 1;

OY 4 CTCGSEDFHSRDVAAIHCGHTFHLOCLIQWFEFAFSRTCPQCRIOY 50
DB 172 CAICFOEFKTEGKREVAATLLCGHEFDNCKIMEMFV--RYNCPICRFEL 216

RESULT 28
O9XUM8 PRELIMINARY; PRT; 489 AA.

AC O9XUM8;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE W02A11.3 PROTEIN.
GN W02A11.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;

OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;

RN [1]
RP SEQUENCE FROM N.A.
RA White S.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;

RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RT Science 282:2012-2018(1998).
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.

DR EMBL: Z82062; CAB04890.1; -.
DR InterPro: IPR001841; Znf_1ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Zinc-finger.
SQ SEQUENCE 489 AA; 54865 MW; 68DFACD078F6A540 CRC64;

Query Match 36.9%; Score 108; DB 5; Length 489;
Best Local Similarity 29.8%; Pred. No. 2.2e-06;
Matches 14; Conservative 12; Mismatches 19; Indels 2; Gaps 1;

OY 4 CTCGSEDFHSRDVAAIHCGHTFHLOCLIQWFEFAFSRTCPQCRIOY 50
DB 433 CTVCLSSEFDEGESIQKLRCHNVHFPECTYKWDI--NKRCPMKREI 477

RESULT 29
O9NSR1 PRELIMINARY; PRT; 137 AA.

AC O9NSR1;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOTHETICAL 15.7 KDA PROTEIN (LIKELY ORTHOLOG OF MOUSE ARKADIA).
GN DKFZP761D081.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=AMYGDALA;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Weil B., Wiemann S.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [12]

RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN, PRIMITIVE NEUROECTODERMAL;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL: AL157474; CAB75669.1; -.
DR EMBL: BC010369; AAH10369.1; -.
DR InterPro: IPR001841; Znf_1ring.
DR Pfam: PF00097; zf-C3HC4; 1.
DR SMART: SM00184; RING; 1.
KW Hypothetical protein; zinc-finger.
SQ SEQUENCE 137 AA; 15739 MW; 6AA62DC6CEB8C114 CRC64;

Query Match 36.5%; Score 107; DB 4; Length 137;
Best Local Similarity 38.3%; Pred. No. 8.5e-07;
Matches 18; Conservative 7; Mismatches 20; Indels 2; Gaps 1;

OY 4 CTCGSEDFHSRDVAAIHCGHTFHLOCLIQWFEFAFSRTCPQCRIOY 50
DB 85 CTCICSLIEGEDVVRRLPCMHLEFHVQCVDDQLIT--NKKCPICRVDI 129

RESULT	30			
Q9FM98				
ID	Q9FM98	PRELIMINARY;	PRT;	396 AA.
AC	Q9FM98;			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, last sequence update)		
DT	01-DEC-2001	(TREMBLrel. 19, last annotation update)		
DE	GENOMIC DNA, CHROMOSOME 5, P1 CLONE:IMCD7.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eurariyola: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
CC	Spermatophyta; Magnoliophyta: eudicotyledons: core eudicots; Rosidae			
OC	eucotsids. II: Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=COLUMBIA;			
RX	MEDLINE=98290546; PubMed=9628582;			
RA	Sato S., Kaneko T., Kotani H., Nakamura Y., Asamizu E., Miyajima N.,			
RA	Tabata S.;			
RT	"Structural analysis of Arabidopsis thaliana chromosome 5. IV. RT			
RT	Sequence features of the regions of 1,456,315 bp covered by nineteen			
RT	physically assigned P1 and TAC clones.";			
CC	DNA Res. 5:41-54(1998)			
CC	-I- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
DR	EMBL; AB009049; BABI1261.1; "			
DR	InterPro: IPR001841; Znf_fing.			
DR	Pfam: PF00097; zf-C3HC4.1.			
DR	SMART: SM00184; RING. 1.			
DR	Zinc-finger.			
QO	SEQUENCE 396 AA; 44359 MW; 43059E73B4442FFB CRC64;			

[illegible]

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008109      31
ID      008109      PDBLIMINARY;      PRT;      551 AA.
AC      008109;
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT      01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE      CHROMOSOME XV READING FRAME ORF Y0L013C.
CN      HRD1 OR Y0L013C.
CS      Saccharomyces cerevisiae (Baker's yeast).
CC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacchar-
OC      Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX      NCBI_TaxID=4932;
      [1]
RN      SEQUENCE FROM N.A.
RP      Hughes B., Pohl T.M.;
RL      Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RL      MIPS;
RA      Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases
CC      -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR      EMBL; 274755; CAA99012.1; -.
DR      SGD; S0005373; HRD1.
DR      InterPro; IPR001841; znf_rlng.
DR      Pfam; PF000097; zf-C3HC4_1.
DR      SMART; SM00184; RING; 1.
KW      Zinc-finger.
KW      SEQUENCE 551 AA; 63534 MW; CAA6341E7A94DB0B CRC64;

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Query Match 36.5%; Score 107; DB 3; Length 551;

Best Local Similarity	37.3%	Pred. No.	3.4e-06;
Matches	22;	Conservative	6;
		Mismatches	19;
		Indels	12;
		Gaps	2;

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QY      2 SLCTICSDFFHDS-----RDVAALHCHTFHQCLLIOWFETAPSRTCPCQRIV 50
          ::||| | : ||| ||| | :||| ||: |
Db    347 NICLICMDELHSPNQQTWKNKNNKKPKRLPCGHILHSCLKMMMER--SQTCPICRLPV 403
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RESULT	32			
090278				
ID	090278	PRELIMINARY;	PRT;	879 AA.
AC	090278;			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	RING FINGER PROTEIN (FRAGMENT).			
GN	ARKADIA.			
OS	Gallus gallus (Chicken).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.			
OX	NCBI_TaxID=9031;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21195971; Pubmed=11298452;			
RA	Episkopou V., Arkell R., Timmons P.M., Walsh J.J., Andrew R.L.,			
RA	Swan D.;			
RT	"Induction of the mammalian node requires Arkadia function in the			
RT	extraembryonic lineages.";			
RL	Nature 410:825-830(2001).			
DR	EMBL: AF329846; AAK38636.1; .			
FT	NON_TER			
EQ	SEQUENCE 879 AA; 95701 MW; EC8564B2280E3264 CRC64;			

Query Match	36.5%;	Score 107;	DB 13;	length 879;
Best Local Similarity	38.3%;	Pred. No. 5.4e-06;		
Matches 18;	Conservative 7;	Mismatches 20;	Indels 2;	Gaps 1;

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QY      4 CTICSDFFDHSRDVAAIHCGHTFHLQCLIQWFETAPSRTPCQRIQV 50
      ||| : ||| : ||| : ||| : ||| :
Db    827 CTICSLIEGEDVRRLLPCMHLFHQVCVDQWLIT--NKKCPICRAVDI 871

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RESULT	33		
090ZT7			
ID	Q90ZT7	PRELIMINARY;	PRT; 923 AA.
AC	Q90ZT7;		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	RING FINGER-H2 PROTEIN (FRAGMENT).		
CN	ARKADIA.		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae;		
OC	Xenopodidae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE-21195971; PubMed-11298452;		
RA	Episkopou V., Arkell R., Timmons P.M., Walsh J.J., Andrew R.L.,		
RA	Swan D.;		
RT	"Induction of the mammalian node requires Arkadia function in the		
RT	extraembryonic lineages.";		
RL	Nature 410:825-830(2001).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RA	Niederlaender C., Walsh J., Episkopou V., Jones M.;		
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.		
DT	EMBL; AF329847; AAK3637.1; -.		
NC	NON_TER		
Q0	SEQUENCE 923 AA: 101298 MW A93CBDA3E05787C CRC64:		

Query Match 36.5%; Score 107; DB 3; Length 551;

OY 1 LSLCTICDFHSDRDVAIHCCTPHLQCLIQWFTAPSRCPQCR 47
 DB 257 LPTCAVCLERNDDSD-VLATICNHSFHARCLEQWAD-----NTGCVCR 297
 RESULT 40
 OYVGI6 PRELIMINARY; PRT; 1256 AA.
 AC OYVGI6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
 DE CG6923 PROTEIN (LD22771p).
 GS CG6923.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BREKLEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-U., Andrews-Planck C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Broksrein P., Brothier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spralling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Y, CN BW SP;
 RA Stapleton M., Broksrein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
 DR EMBL; AE003692; AAF54693.1; -;
 DR EMBL; AY058520; AAL13749.1; -;

DR HSSP; P28990; ICHC.
 DR FlyBase; FBgn0037944; CG6923.
 DR InterPro; IPR001841; znf_ring.
 DR Pfam; PF00097; zf-C3HC4; 1.
 DR SMART; SM00184; RING; 1.
 KW Zinc-finger.
 SQ SEQUENCE 1256 AA; 138666 MW; 17FA760165507EAE CRC64;
 OY 4 CTICSDFFHSDRDVAIHCCTPHLQCLIQWFTAPSRCPQCRIOV 50
 DB 1187 CAICLNLFEIENEYRRPLPCMLHRTDCVDMVLT--NKHCPICRVPI 1231
 Query Match 35.8%; Score 105; DB 5; Length 1256;
 Best Local Similarity 36.2%; Pred. No. 1.4e-05;
 Matches 17; Conservative 9; Mismatches 19; Indels 2; Gaps 1;

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 Job time: 1493 sec

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